Project Report: Genomic determinants of parasitism and mutualism in bacterial endosymbioses

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Project Progress

We are studying the genetic assimilation events that fashion different prokaryotic–eukaryotic endosymbioses, i.e., mutualism and reproductive parasitism, using the most abundant bacterial endosymbiont on the planet, *Wolbachia* . Our findings have important Astrobiology implications, including insights into small life (bacteriophages and the highly–reduced bacterial genomes of endosymbionts), genome integration, organismal complexity, the evolution of interkingdom associations, and the adaptations of prokaryotic life in a confined environment – the eukaryotic cytoplasm. In this past year, we have taken our original research objectives farther than expected. We generated new genomic data described in imminent publications on lateral transfer and recombination of an active bacteriophage in the parasitic *Wolbachia* . From this work, we developed a novel hypothesis on the exchange of genetic information between intracellular microbial communities, termed the intracellular arena hypothesis; and we showed that bacteriophage elements not only transfer themselves between *Wolbachia* parasites, but they also transfer mobile genetic elements onto the host bacterial chromosome. We completed a comprehensive phylogenetic analysis on the origin of endosymbiotic parasitism and mutualism in *Wolbachia* and are now writing up this work. Ongoing work focuses on understanding the genome size and content differences that underlie endosymbiont lifestyles. We are using microarrays to identify the gene loss and acquisition events that occurred during the radiation of this endosymbiosis. We will map these genome changes onto the *Wolbachia* phylogeny to determine when these events occurred and how they associate with lifestyle. Our research is drawing general conlusions about the early genome interactions that shape endosymbioses and genomic integration.

Highlights

- Bacteriophages can be widespread in endosymbionts that show labile transmission patterns and parasitism.
- Bacteriophages are a major source of genetic flux (i.e., recombination, lateral transfer) in some endosymbiont genomes.
- Bacteriophages can shuttle selfish mobile elements, e.g., transposons, onto the host bacterial chromosome of some labile intracellular bacteria.

- Genome sizes of the parasitic *Wolbachia* are variable.

Roadmap Objectives

- ***Objective No. 3.4:*** Origins of cellularity and protobiological systems
- ***Objective No. 4.1:*** Earth's early biosphere
- ***Objective No. 4.2:*** Foundations of complex life
- ***Objective No. 5.1:*** Environment–dependent, molecular evolution in microorganisms
- ***Objective No. 5.2:*** Co–evolution of microbial communities